0420 0360

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PATENT APPLICATION: US/10/034,158

DATE: 01/18/2002
TIME: 08:05:39

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  3 <110> APPLICANT: Wei, Zhong-Min
  5 <120> TITLE OF INVENTION: METHOD OF IMPARTING DROUGHT RESISTANCE TO PLANTS
  7 <130> FILE REFERENCE: 21829/230
  9 <140> CURRENT APPLICATION NUMBER: US/10/034,158
 10 <141> CURRENT FILING DATE: 2001-12-20
 12 <150> PRIOR APPLICATION NUMBER: 09/597,840
 13 <151> PRIOR FILING DATE: 2000-06-20
 15 <150> PRIOR APPLICATION NUMBER: 09/013,587
 16 <151> PRIOR FILING DATE: 1998-01-26
 18 <150> PRIOR APPLICATION NUMBER: 60/036,048
 19 <151> PRIOR FILING DATE: 1997-01-27
 21 <160> NUMBER OF SEQ ID NOS: 10
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 26 <211> LENGTH: 338
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 35              20                  25                  30
 37 Leu Gly Ser Ser Val Asp Lys Leu Ser Ser Thr Ile Asp Lys Leu Thr
 38          35                  40                  45
 40 Ser Ala Leu Thr Ser Met Met Phe Gly Gly Ala Leu Ala Gln Gly Leu
 41      50                  55                  60
 43 Gly Ala Ser Ser Lys Gly Leu Gly Met Ser Asn Gln Leu Gly Gln Ser
 44  65                  70                  75                  80
 46 Phe Gly Asn Gly Ala Gln Gly Ala Ser Asn Leu Leu Ser Val Pro Lys
 47                  85                  90                  95
 49 Ser Gly Gly Asp Ala Leu Ser Lys Met Phe Asp Lys Ala Leu Asp Asp
 50              100                 105                 110
 52 Leu Leu Gly His Asp Thr Val Thr Lys Leu Thr Asn Gln Ser Asn Gln
 53          115                 120                 125
 55 Leu Ala Asn Ser Met Leu Asn Ala Ser Gln Met Thr Gln Gly Asn Met
 56      130                 135                 140
 58 Asn Ala Phe Gly Ser Gly Val Asn Asn Ala Leu Ser Ser Ile Leu Gly
 59 145                 150                 155                 160
 61 Asn Gly Leu Gly Gln Ser Met Ser Gly Phe Ser Gln Pro Ser Leu Gly
 62                  165                 170                 175
 64 Ala Gly Gly Leu Gln Gly Leu Ser Gly Ala Gly Ala Phe Asn Gln Leu
 65              180                 185                 190
 67 Gly Asn Ala Ile Gly Met Gly Val Gly Gln Asn Ala Ala Leu Ser Ala
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74 225                 230                 235                 240
76 Gln Tyr Pro Glu Ile Phe Gly Lys Pro Glu Tyr Gln Lys Asp Gly Trp
77                  245                 250                 255
79 Ser Ser Pro Lys Thr Asp Asp Lys Ser Trp Ala Lys Ala Leu Ser Lys
80              260                 265                 270
82 Pro Asp Asp Asp Gly Met Thr Gly Ala Ser Met Asp Lys Phe Arg Gln
83          275                 280                 285
85 Ala Met Gly Met Ile Lys Ser Ala Val Ala Gly Asp Thr Gly Asn Thr
86      290                 295                 300
88 Asn Leu Asn Leu Arg Gly Ala Gly Gly Ala Ser Leu Gly Ile Asp Ala
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106 gatctggtat ttcagtttgg ggacaccggg cgtgaactca tgatgcagat tcagccgggg 180
107 cagcaatatc ccggcatgtt gcgcacgctg ctcgctcgtc gttatcagca ggcggcagag 240
108 tgcgatggct gccatctgtg cctgaacggc agcgatgtat tgatcctctg gtggccgctg 300
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110 acgttgccgt cgctatccat agcaccgacg gcgcgtccgc agacagggaa cggacgcgcc 420
111 cgatcattaa gataaaggcg gctttttta ttgcaaaacg gtaacggtga ggaaccgttt 480
112 caccgtcggc gtcactcagt aacaagtatc catcatgatg cctacatcgg gatcggcgtg 540
113 ggcatccgtt gcagatactt ttgcgaacac ctgacatgaa tgaggaaacg aaattatgca 600
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128 cgccagcatg gacaaattcc gtcaggcgat gggtatgatc aaaagcgcgg tggcgggtga 1500
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132 ttattatgcg gtttatgcgg ttacctggac cggttaatca tcgtcatcga tctggtacaa 1740
133 acgcacattt tcccgttcat tcgcgtcgtt acgcgccaca atcgcgatgg catcttcctc 1800
134 gtcgctcaga ttgcgcggct gatggggaac gccgggtgga atatagagaa actcgccggc 1860
135 cagatggaga cacgtctgcg ataaatctgt gccgtaacgt gtttctatcc gccccctttag 1920
136 cagatagatt gcggtttcgt aatcaacatg gtaatgcggt tccgcctgtg cgccggccgg 1980
137 gatcaccaca atattcatag aaagctgtct tgcacctacc gtatcgcggg agataccgac 2040
138 aaaatagggc agtttttgcg tggtatccgt ggggtgttcc ggcctgacaa tcttgagttg 2100
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152             20                  25                  30
154 Asn Ala Gly Leu Gly Gly Asn Ser Ala Leu Gly Leu Gly Gly Gly Asn
155         35                  40                  45
157 Gln Asn Asp Thr Val Asn Gln Leu Ala Gly Leu Leu Thr Gly Met Met
158     50                  55                  60
160 Met Met Met Ser Met Met Gly Gly Gly Gly Leu Met Gly Gly Gly Leu
161 65                  70                  75                  80
163 Gly Gly Gly Leu Gly Asn Gly Leu Gly Gly Ser Gly Gly Leu Gly Glu
164                 85                  90                  95
166 Gly Leu Ser Asn Ala Leu Asn Asp Met Leu Gly Gly Ser Leu Asn Thr
167             100                 105                 110
169 Leu Gly Ser Lys Gly Gly Asn Asn Thr Thr Ser Thr Thr Asn Ser Pro
170         115                 120                 125
172 Leu Asp Gln Ala Leu Gly Ile Asn Ser Thr Ser Gln Asn Asp Asp Ser
173     130                 135                 140
175 Thr Ser Gly Thr Asp Ser Thr Ser Asp Ser Ser Asp Pro Met Gln Gln
176 145                 150                 155                 160
178 Leu Leu Lys Met Phe Ser Glu Ile Met Gln Ser Leu Phe Gly Asp Gly
179                 165                 170                 175
181 Gln Asp Gly Thr Gln Gly Ser Ser Ser Gly Gly Lys Gln Pro Thr Glu
182             180                 185                 190
184 Gly Glu Gln Asn Ala Tyr Lys Lys Gly Val Thr Asp Ala Leu Ser Gly
185         195                 200                 205
187 Leu Met Gly Asn Gly Leu Ser Gln Leu Leu Gly Asn Gly Gly Leu Gly
188     210                 215                 220
190 Gly Gly Gln Gly Gly Asn Ala Gly Thr Gly Leu Asp Gly Ser Ser Leu
191 225                 230                 235                 240
193 Gly Gly Lys Gly Leu Gln Asn Leu Ser Gly Pro Val Asp Tyr Gln Gln
194                 245                 250                 255
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206 305                 310                 315                 320
208 Gly Gln Glu Val Lys Thr Asp Asp Lys Ser Trp Ala Lys Ala Leu Ser
209             325                 330                 335
211 Lys Pro Asp Asp Asp Gly Met Thr Pro Ala Ser Met Glu Gln Phe Asn
212             340                 345                 350
214 Lys Ala Lys Gly Met Ile Lys Arg Pro Met Ala Gly Asp Thr Gly Asn
215         355                 360                 365
217 Gly Asn Leu Gln Ala Arg Gly Ala Gly Gly Ser Ser Leu Gly Ile Asp
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236 ggtggcaatt ctgcactggg gctgggcggc ggtaatcaaa atgataccgt caatcagctg 240
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259 <212> TYPE: PRT
260 <213> ORGANISM: Pseudomonas syringae
262 <400> SEQUENCE: 5
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270          35                  40                  45
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273      50                  55                  60
275 Lys Ser Met Ala Ala Asp Gly Lys Ala Gly Gly Gly Ile Glu Asp Val
276  65                  70                  75                  80
278 Ile Ala Ala Leu Asp Lys Leu Ile His Glu Lys Leu Gly Asp Asn Phe
279                  85                  90                  95
281 Gly Ala Ser Ala Asp Ser Ala Ser Gly Thr Gly Gln Gln Asp Leu Met
282             100                 105                 110
284 Thr Gln Val Leu Asn Gly Leu Ala Lys Ser Met Leu Asp Asp Leu Leu
285         115                 120                 125
287 Thr Lys Gln Asp Gly Gly Thr Ser Phe Ser Glu Asp Asp Met Pro Met
288     130                 135                 140
290 Leu Asn Lys Ile Ala Gln Phe Met Asp Asp Asn Pro Ala Gln Phe Pro
291 145                 150                 155                 160
293 Lys Pro Asp Ser Gly Ser Trp Val Asn Glu Leu Lys Glu Asp Asn Phe
294                 165                 170                 175
296 Leu Asp Gly Asp Glu Thr Ala Ala Phe Arg Ser Ala Leu Asp Ile Ile
297             180                 185                 190
299 Gly Gln Gln Leu Gly Asn Gln Gln Ser Asp Ala Gly Ser Leu Ala Gly
300         195                 200                 205
302 Thr Gly Gly Gly Leu Gly Thr Pro Ser Ser Phe Ser Asn Asn Ser Ser
303     210                 215                 220
305 Val Met Gly Asp Pro Leu Ile Asp Ala Asn Thr Gly Pro Gly Asp Ser
306 225                 230                 235                 240
308 Gly Asn Thr Arg Gly Glu Ala Gly Gln Leu Ile Gly Glu Leu Ile Asp
309                 245                 250                 255
311 Arg Gly Leu Gln Ser Val Leu Ala Gly Gly Gly Leu Gly Thr Pro Val
312             260                 265                 270
314 Asn Thr Pro Gln Thr Gly Thr Ser Ala Asn Gly Gly Gln Ser Ala Gln
315         275                 280                 285
317 Asp Leu Asp Gln Leu Leu Gly Gly Leu Leu Leu Lys Gly Leu Glu Ala
318     290                 295                 300
320 Thr Leu Lys Asp Ala Gly Gln Thr Gly Thr Asp Val Gln Ser Ser Ala
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331 <211> LENGTH: 1026
332 <212> TYPE: DNA
333 <213> ORGANISM: Pseudomonas syringae
335 <400> SEQUENCE: 6
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VERIFICATION SUMMARY DATE: 01/18/2002
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L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date